

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RICCARDI, Carlo
- (ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 - (B) STREET: 624 Ninth Street, N.W., Suite 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/403,861
 - (B) FILING DATE: 11-FEB-2000
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP98/02490
 - (B) FILING DATE: 27-APR-1998
- vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 97107033.9
 - (B) FILING DATE: 28-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: YUN, Allen C.
 - (B) REGISTRATION NUMBER: 37,971
 - (C) REFERENCE/DOCKET NUMBER: RICCARDI=1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:206..616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC	60
TCCAGCTTAG AAGTGCCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG	120
GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA	180
GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC	232
Met Asn Thr Glu Met Tyr Gln Thr Pro	
1 5	
ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT	280
Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe	
10 15 20 25	
TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT	328
Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser	
30 35 40	
GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC	376
Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala	
45 50 55	
ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG	424
Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val	
60 65 70	
GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG	472
Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln	
75 80 85	
CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA	520
Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln	
90 95 100 105	
CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA	568
Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu	
110 115 120	
GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG	616
Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val	
125 130 135	
TAAGTGGCTC TGTCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG	676
TTTGTTTTTG GCTCCCAAG GGTCACTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG	736
TGCCAAGAGA TGTCCCAAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC	796
AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC	856
TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA	916
GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT	976
TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCTT ATGAAGAAGC	1036

CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG 1096
CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG 1156
GCTTTGTGCA CAGCCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT 1216
TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC 1276
TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTGAAGGG 1336
CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTGGACTG 1396
TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG 1456
AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC 1516
TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT 1576
GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA 1636
GTTTTAGGTT GTTTTTTTTT GGTTTTGTGT GTTTGTTTGT TTGTTTGTGT TGTTTTTTTG 1696
TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT 1756
GGTAGACCAG AGGAGTAACT AGTTTTGATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG 1816
CTTGTTGTAAG GAGGTTCTGT GACAGTGAAC ACTTCCACT TTCTGACACC TCATCCTGCT 1876
GTACGACTCC AGGATTGGA TTTGGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT 1936
TGCTCCTTTT TCTAAAAATA AAAAAAAAAA AAAAAA 1972

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
1 5 10 15
Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
20 25 30
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
35 40 45
Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
50 55 60
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
65 70 75 80
Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
85 90 95

Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg
 100 105 110
 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr
 115 120 125
 Pro Glu Ala Pro Gly Gly Ser Ala Val
 130 135

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /note= "PCR forward primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /note= "PCR reverse primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTGG GAGTGGCACC

20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:241..642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC	60
AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCCTCCT	120
AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC	180
AGCCGCCCAG CCGCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC	240
ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln	288
5 10 15	
CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp	336
20 25 30	
GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val	384
35 40 45	
GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His	432
50 55 60	
CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile	480
65 70 75 80	
CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu	528
85 90 95	
TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys	576
100 105 110	
CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala	624
115 120 125	
CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCTCAGG GTGGGCAGAG Pro Gly Gly Ser Ala Val	672
130	
CCACTAAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT	732
CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC	792
ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC	852
ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC	912

AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC 972
 AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT 1032
 TCACCTGACA ACGACTGTTC CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC 1092
 TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA 1152
 GCCTTCTGTT GGTTAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA 1212
 CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTAG TATTGGCATA GTTTTCTAT 1272
 ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT 1332
 ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACC AGCCTTGGA GTATTGACTG 1392
 GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTCA TTACCAAGTT GACCCAGTTT 1452
 GTCTTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT 1512
 GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCAGC TGTCCACTGA AACGTGAAGT 1572
 CCTGTTTTGA ATGCCAAACC CACCATTAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG 1632
 AAGATCAGTT TGGGCTTCAC AGTGTCAATTT GAAAAAGCGT TTTTGTTTTG TTTGAATTA 1692
 TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCTTA CTGTGGATGA GGGATGAACA 1752
 AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG 1812
 GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG 1872
 GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCA ATAACTTTG CTCTGTTTTT 1932
 CTAAAAAATA AAAA 1946

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
 1 5 10 15
 Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
 20 25 30
 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
 35 40 45
 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
 50 55 60
 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile

65	70	75	80
Arg Glu Leu Val	Glu Lys Asn Ser Gln	Leu Glu Arg Glu	Asn Thr Leu
	85	90	95
Leu Lys Thr Leu	Ala Ser Pro Glu	Gln Leu Glu Lys	Phe Gln Ser Cys
	100	105	110
Leu Ser Pro Glu	Glu Pro Ala Pro	Glu Ser Pro Gln	Val Pro Glu Ala
	115	120	125
Pro Gly Gly Ser	Ala Val		
	130		

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: pepetide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Lys Glu Gln	Ile Lys Glu Leu	Ile Glu Lys Asn	Ser Gln Leu Glu
1	5	10	15
Gln Glu Asn Asp	Leu Leu Lys Thr	Leu Ala	
	20	25	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Glu Asp Lys	Val Glu Glu Leu	Leu Ser Lys Asn	Tyr His Leu Glu
1	5	10	15
Asn Glu Val Ala	Arg Leu Lys Lys	Leu Val	
	20	25	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile

1	5	10	15
Glu	Glu	Leu	Lys
	Ala	Leu	Lys
		Asp	Leu
			Tyr
	20	25	

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu	Glu	Asn	Arg	Val	Ala	Val	Leu	Glu	Asn	Gln	Asn	Lys	Thr	Leu	Ile
1				5				10						15	

Glu	Glu	Leu	Lys	Ala	Leu	Lys	Asp	Leu	Tyr
								20	25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu	Glu	Glu	Lys	Val	Lys	Thr	Leu	Lys	Ala	Gln	Asn	Ser	Glu	Leu	Ala
1				5				10						15	

Ser	Thr	Ala	Asn	Met	Leu	Arg	Glu	Gln	Val
				20				25	

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Asp	Leu	Val	Lys	Asn	His	Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val
1				5				10						15	

Glu	Ile	Leu	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Val	Glu	Lys	Asn	Ser	Gln
				20				25					30		

Leu	Glu	Arg	Glu	Asn	Thr	Leu	Leu	Lys	Thr	Leu	Ala	Ser	Pro	Glu	Gln
				35				40					45		

Leu Glu Lys Phe Gln Ser Cys Leu Ser Pro Glu Glu Pro Ala Pro Glu
50 55 60
Ser Pro Gln Val Pro Glu Ala Pro Gly Gly Ser Ala Val
65 70 75

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr Gln
1 5 10 15
Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr Glu
20 25 30
Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val Val
35 40 45
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser His
50 55 60
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
65 70 75 80
Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn Leu
85 90 95
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala Gln
100 105 110
Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr Thr
115 120 125
Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Glu Val Asp

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with $\text{CH}_2\text{OC}(\text{O}) - [2,6 - (\text{CF}_3)_2]\text{Ph}$ "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Tyr Val Ala Asp